



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/749,728A  
 Source: OIPE  
 Date Processed by STIC: 2/8/2002

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

**Raw Sequence Listing Error Summary**

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/749,728A</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 3 <sup>rd</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <u>80 and more</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/749,728A

DATE: 02/08/2002  
TIME: 11:44:39

Input Set : A:\766.43 Sequence Listing.txt  
Output Set: N:\CRF3\02082002\I749728A.raw

ppr 1-4

3 <110> APPLICANT: Umezawa, Akihiro  
4 Hata, Jun-Ichi  
5 Fukuda, Keiichi  
6 Ogawa, Satoshi  
7 Sakurada, Kazuhiro  
8 Gojo, Satoshi  
9 Yamada, Yoji

11 <120> TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO  
CARDIOMYOCYTES

13 <130> FILE REFERENCE: 00766.000043  
15 <140> CURRENT APPLICATION NUMBER: US/09/749,728A  
16 <141> CURRENT FILING DATE: 2001-09-17  
18 <150> PRIOR APPLICATION NUMBER: H11-372826  
19 <151> PRIOR FILING DATE: 1999-12-28  
21 <150> PRIOR APPLICATION NUMBER: PCT-JP00-01148  
22 <151> PRIOR FILING DATE: 2000-02-28  
24 <150> PRIOR APPLICATION NUMBER: PCT-JP00-07741  
25 <151> PRIOR FILING DATE: 2000-11-02  
27 <160> NUMBER OF SEQ ID NOS: 80  
29 <170> SOFTWARE: PatentIn Ver.2.0

Does Not Comply  
Corrected Diskette Needed

## ERRORED SEQUENCES

②

343 <210> SEQ ID NO: 7  
344 <211> LENGTH: 155  
345 <212> TYPE: PRT  
346 <213> ORGANISM: Homo sapiens  
N-> 347 <400> SEQUENCE: 7  
348 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly  
349 1 5 10 15  
350 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu  
351 20 25 30  
352 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg  
353 35 40 45  
354 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu  
355 50 55 60  
356 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn  
357 65 70 75 80  
358 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys  
359 85 90 95  
360 Val Thr Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr  
361 100 105 110  
362 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/749,728A

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Input Set : A:\766.43 Sequence Listing.txt  
Output Set: N:\CRF3\02082002\I749728A.raw

363 115 120 125  
364 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys  
365 130 135 140  
366 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser  
E--> 367 145 150 155 *insert*  
850 <210> SEQ ID NO: 15  
851 <211> LENGTH: 365  
852 <212> TYPE: PRT  
853 <213> ORGANISM: Homo sapiens  
OK> 854 <400> SEQUENCE: 15  
855 Met Gly Arg Lys Lys Ile Gln Ile Ser Arg Ile Leu Asp Gln Arg Asn  
856 1 5 10 15  
857 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala  
858 20 25 30  
859 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe  
860 35 40 45  
861 Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg  
862 50 55 60  
863 Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr  
864 65 70 75 80  
865 Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp  
866 85 90 95  
867 Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys  
868 100 105 110  
869 Phe Arg Arg Leu Ala Gly Glu Gly Asp Pro Ala Leu Pro Arg Pro  
870 115 120 125  
871 Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr  
872 130 135 140  
873 Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala  
874 145 150 155 160  
875 Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys  
876 165 170 175  
877 Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu  
878 180 185 190  
879 Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg  
880 195 200 205  
881 Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr  
882 210 215 220  
883 Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr  
884 225 230 235 240  
885 Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro  
886 245 250 255  
887 Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro  
888 260 265 270  
889 Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg  
890 275 280 285  
891 Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys  
892 290 295 300  
893 Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/749,728A

DATE: 02/08/2002  
TIME: 11:44:40

Input Set : A:\766.43 Sequence Listing.txt  
Output Set: N:\CRF3\02082002\I749728A.raw

894	305	310	315	320												
895	Ala	Gly	Cys	Pro	Trp	Pro	Thr	Ala	Gly	Pro	Gly	Arg	Arg	Ser	Pro	Gly
896							325		330						335	
897	Gly	Thr	Ser	Pro	Glu	Arg	Ser	Pro	Gly	Thr	Ala	Arg	Ala	Arg	Gly	Asp
898							340		345						350	
899	Pro	Thr	Ser	Leu	Gln	Ala	Ser	Ser	Glu	Lys	Thr	Gln	Gln			
E--> 900							355		360						365	←
1401	<210> SEQ ID NO: 23															
1402	<211> LENGTH: 215															
1403	<212> TYPE: PRT															
1404	<213> ORGANISM: Homo sapiens															
W--> 1405	<400> SEQUENCE: 23															
1406	Met	Asn	Leu	Val	Gly	Ser	Tyr	Ala	His	His	His	His	His	His	Pro	
1407								1	5	10	15					
1408	His	Pro	Ala	His	Pro	Met	Leu	His	Glu	Pro	Phe	Leu	Phe	Gly	Pro	Ala
1409							20		25					30		
1410	Ser	Arg	Cys	His	Gln	Glu	Arg	Pro	Tyr	Phe	Gln	Ser	Trp	Leu	Leu	Ser
1411							35		40					45		
1412	Pro	Ala	Asp	Ala	Ala	Pro	Asp	Phe	Pro	Ala	Gly	Gly	Pro	Pro	Pro	Ala
1413							50		55					60		
1414	Ala	Ala	Ala	Ala	Ala	Thr	Ala	Tyr	Gly	Pro	Asp	Ala	Arg	Pro	Gly	Gln
1415							65		70					80		
1416	Ser	Pro	Gly	Arg	Leu	Glu	Ala	Leu	Gly	Gly	Arg	Leu	Gly	Arg	Arg	Lys
1417							85		90					95		
1418	Gly	Ser	Gly	Pro	Lys	Lys	Glu	Arg	Arg	Arg	Thr	Glu	Ser	Ile	Asn	Ser
1419							100		105					110		
1420	Ala	Phe	Ala	Glu	Leu	Arg	Glu	Cys	Ile	Pro	Asn	Val	Pro	Ala	Asp	Thr
1421							115		120					125		
1422	Lys	Leu	Ser	Lys	Ile	Lys	Thr	Leu	Arg	Leu	Ala	Thr	Ser	Tyr	Ile	Ala
1423							130		135					140		
1424	Tyr	Leu	Met	Asp	Val	Leu	Ala	Lys	Asp	Ala	Gln	Ser	Gly	Asp	Pro	Glu
1425							145		150					155		160
1426	Ala	Phe	Lys	Ala	Glu	Leu	Lys	Lys	Ala	Asp	Gly	Gly	Arg	Glu	Ser	Lys
1427							165		170					175		
1428	Arg	Lys	Arg	Glu	Leu	Gln	Gln	His	Glu	Gly	Phe	Pro	Pro	Ala	Leu	Gly
1429							180		185					190		
1430	Pro	Val	Glu	Lys	Arg	Ile	Lys	Gly	Arg	Thr	Gly	Trp	Pro	Gln	Gln	Val
1431							195		200					205		
1432	Trp	Ala	Leu	Glu	Leu	Asn	Gln									
E--> 1433							210		215	←						
2651	<210> SEQ ID NO: 63															
2652	<211> LENGTH: 215															
2653	<212> TYPE: PRT															
2654	<213> ORGANISM: Homo sapiens															
W--> 2655	<400> SEQUENCE: 63															
2656	Met	Gly	Ser	Pro	Arg	Ser	Ala	Leu	Ser	Cys	Leu	Leu	Leu	His	Leu	Leu
2657							1	5			10			15		
2659	Val	Leu	Cys	Leu	Gln	Ala	Gln	Val	Thr	Val	Gln	Ser	Ser	Pro	Asn	Phe
2660							20		25					30		

P.4

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/749,728A

DATE: 02/08/2002  
TIME: 11:44:40

Input Set : A:\766.43 Sequence Listing.txt  
Output Set: N:\CRF3\02082002\I749728A.raw

2662 Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg  
2663 35 40 45  
2665 Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His  
2666 50 55 60  
2668 Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly  
2669 65 70 75 80  
2671 Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg  
2672 85 90 95  
2674 Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys  
2675 100 105 110  
2677 Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val  
2678 115 120 125  
2680 Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala  
2681 130 135 140  
2683 Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg  
2684 145 150 155 160  
2686 Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys  
2687 165 170 175  
2689 Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu  
2690 180 185 190  
2692 Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg  
2693 195 200 205  
2695 Thr Trp Ala Pro Glu Pro Arg  
E--> 2696 210 215 *l*  
3200 <210> SEQ ID NO: 80  
3201 <211> LENGTH: 19  
3202 <212> TYPE: DNA  
3203 <213> ORGANISM: Artificial Sequence  
W--> 3204 <220> FEATURE:  
W--> 3204 <223> OTHER INFORMATION:  
W--> 3204 <400> SEQUENCE: 80  
3205 gggtgctcaq gtatgtggtt  
E--> 3208 *my main 231957v1* *delete*

*see item 11 on Error Summary sheet*

The types of errors shown exist throughout the Sequence Listing. Please check <sup>19</sup> all sequences for similar errors.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/749,728A

DATE: 02/08/2002  
TIME: 11:44:41

Input Set : A:\766.43 Sequence Listing.txt  
Output Set: N:\CRF3\02082002\I749728A.raw

L:35 M:283 W: Missing Blank Line separator, <400> field identifier  
L:92 M:283 W: Missing Blank Line separator, <220> field identifier  
L:95 M:283 W: Missing Blank Line separator, <400> field identifier  
L:178 M:283 W: Missing Blank Line separator, <400> field identifier  
L:209 M:283 W: Missing Blank Line separator, <220> field identifier  
L:212 M:283 W: Missing Blank Line separator, <400> field identifier  
L:256 M:283 W: Missing Blank Line separator, <400> field identifier  
L:292 M:283 W: Missing Blank Line separator, <220> field identifier  
L:295 M:283 W: Missing Blank Line separator, <400> field identifier  
L:347 M:283 W: Missing Blank Line separator, <400> field identifier  
L:367 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
L:372 M:283 W: Missing Blank Line separator, <220> field identifier  
L:375 M:283 W: Missing Blank Line separator, <400> field identifier  
L:410 M:283 W: Missing Blank Line separator, <400> field identifier  
L:457 M:283 W: Missing Blank Line separator, <220> field identifier  
L:460 M:283 W: Missing Blank Line separator, <400> field identifier  
L:528 M:283 W: Missing Blank Line separator, <400> field identifier  
L:589 M:283 W: Missing Blank Line separator, <220> field identifier  
L:592 M:283 W: Missing Blank Line separator, <400> field identifier  
L:681 M:283 W: Missing Blank Line separator, <400> field identifier  
L:750 M:283 W: Missing Blank Line separator, <220> field identifier  
L:753 M:283 W: Missing Blank Line separator, <400> field identifier  
L:854 M:283 W: Missing Blank Line separator, <400> field identifier  
L:900 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15  
L:905 M:283 W: Missing Blank Line separator, <220> field identifier  
L:908 M:283 W: Missing Blank Line separator, <400> field identifier  
L:982 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1046 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1049 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1144 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1215 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1218 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1322 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1355 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1358 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1405 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1433 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23  
L:1438 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1441 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1488 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1545 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1548 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1631 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1690 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1693 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1779 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1839 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1842 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/749,728A

DATE: 02/08/2002  
TIME: 11:44:41

Input Set : A:\766.43 Sequence Listing.txt  
Output Set: N:\CRF3\02082002\I749728A.raw

L:1931 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2078 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2081 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2299 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2301 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2696 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:63  
L:3141 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3141 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3148 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3148 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3155 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3155 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3162 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3162 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3169 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3169 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3176 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3176 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3183 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3183 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3190 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3190 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3197 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3197 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3204 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3204 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:3208 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:80  
L:3208 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:80  
L:3208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80  
L:3208 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:27 SEQ:80  
L:3208 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
L:3208 M:112 C: (48) String data converted to lower case,  
L:3208 M:252 E: No. of Seq. differs, <211>LENGTH:Input:19 Found:27 SEQ:80